

# SEQUENCE LISTING

<110> Curiel, David T.  
 Krasnykh, Victor N.  
 <120> Modified Adenovirus Containing A Fiber  
 Replacement Protein  
 <130> D6070CIP  
 <141> 2000-07-10  
 <150> US 09/250,580  
 US 60/074,844  
 <151> 1999-02-16  
 1998-02-17  
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 <223> Forward primer FF.F used to amplify segment of the T4  
 fibritin gene encoding amino acids Ser-229 through  
 the carboxy terminal Ala-487.  
 <400> 1  
 gggaacttga cctcacagaa cgtttatagt cgtttaaagt 40  
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 the carboxy terminal Ala-487.  
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 gggccaatat t 61

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 <212> DNA  
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 <223> primer to PCR amplify FF/6H in pXK.FF/6H

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ccctcatgaa gcgcgcaaga ccgtctg 27

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<210> 11  
<211> 8  
<212> PRT  
<213> Adenovirus type 5  
<220>  
<221> DOMAIN  
<223> the beginning of the third pseudorepeat of the  
fiber shaft domain  
<400> 11

Gly Asn Thr Leu Ser Gln Asn Val  
5 8

<210> 12  
<211> 26  
<212> PRT  
<213> Phage T4  
<220>  
<221> DOMAIN  
<223> the sixth coiled coil segment of the  $\alpha$ -helical  
central domain of the fibritin  
<400> 12

Val Tyr Ser Arg Leu Asn Glu Ile Asp Thr Lys Gln Thr Thr Val  
5 10 15

Glu Ser Asp Ile Ser Ala Ile Lys Thr Ser Ile  
 20 25

<210> 13  
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 <212> PRT  
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 <221> CHAIN  
 <223> the fiber-fibritin-6H chimera  
 <400> 13

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Pro	Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	20	25	30
Pro	Pro	Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	35	40	45
Val	Leu	Ser	Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	50	55	60
Met	Ala	Leu	Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	65	70	75
Asn	Leu	Thr	Ser	Gln	Asn	Val	Tyr	Ser	Arg	Leu	Asn	Glu	Ile	Asp	80	85	90
Thr	Lys	Gln	Thr	Thr	Val	Glu	Ser	Asp	Ile	Ser	Ala	Ile	Lys	Thr	95	100	105
Ser	Ile	Gly	Tyr	Pro	Gly	Asn	Asn	Ser	Ile	Ile	Thr	Ser	Val	Asn	110	115	120
Thr	Asn	Thr	Asp	Asn	Ile	Ala	Ser	Ile	Asn	Leu	Glu	Leu	Asn	Gln	125	130	135
Ser	Gly	Gly	Ile	Lys	Gln	Arg	Leu	Thr	Val	Ile	Glu	Thr	Ser	Ile	140	145	150
Gly	Ser	Asp	Asp	Ile	Pro	Ser	Ser	Ile	Lys	Gly	Gln	Ile	Lys	Asp	155	160	165
Asn	Thr	Thr	Ser	Ile	Glu	Ser	Leu	Asn	Gly	Ile	Val	Gly	Glu	Asn	170	175	180
Thr	Ser	Ser	Gly	Leu	Arg	Ala	Asn	Val	Ser	Trp	Leu	Asn	Gln	Ile			

	185	190	195
Val Gly Thr Asp	Ser Ser Gly Gly Gln	Pro Ser Pro Pro Gly	Ser
	200	205	210
Leu Leu Asn Arg	Val Ser Thr Ile Glu	Thr Ser Val Ser Gly	Leu
	215	220	225
Asn Asn Asp Val	Gln Asn Leu Gln Val	Glu Ile Gly Asn Asn	Ser
	230	235	240
Thr Gly Ile Lys	Gly Gln Val Val Ala	Leu Asn Thr Leu Val	Asn
	245	250	255
Gly Thr Asn Pro	Asn Gly Ser Thr Val	Glu Glu Arg Gly Leu	Thr
	260	265	270
Asn Ser Ile Lys	Ala Asn Glu Thr Asn	Ile Ala Ser Val Thr	Gln
	275	280	285
Glu Val Asn Thr	Ala Lys Gly Asn Ile	Ser Ser Leu Gln Gly	Asp
	290	295	300
Val Gln Ala Leu	Gln Glu Ala Gly Tyr	Ile Pro Glu Ala Pro	Arg
	305	310	315
Asp Gly Gln Ala	Tyr Val Arg Lys Asp	Gly Glu Trp Val Leu	Leu
	320	325	330
Ser Thr Phe Leu	Ser Pro Ala Gly Gly	Gly Gly Ser Gly Gly	Gly
	335	340	345
Gly Ser Gly Gly	Gly Gly Ser Arg Gly	Ser His His His His	His
	350	355	360
His			
361			

<210> 14  
 <211> 9  
 <212> PRT  
 <213> Unknown  
 <220>  
 <221> DOMAIN  
 <223> a peptide ligand containing the RGD motif  
 <400> 14

Cys Asp Cys Arg Gly Asp Cys Phe Cys  
 5 9